

JC10 Rec'd PCT/PTO 23 DEC 2005

SEQUENCE LISTING

SEQ ID NO: 1 - SARS Coronavirus Urbani S-protein full-length gene sequence (AY278741, 3768 bps)

atgtttattttctattttcttactctcactagtggttagtgaccttgaccgggtgcaccactttgatgatgttcaagctcc
taattacactcaacatacttcatctatgaggggggttactatcctgatgaatttttagatcagacactctttatttaactcag
gattatttcttccattttattctaagtgttacagggttcatactattaatcatacgtttggcaaccctgtcataccttttaaggat
ggattatttttctgccacagagaaatcaaatgtgtccgtggttgggttttgggttctacatgaacaacaagtcacagtc
ggtgattattttaacaattctactaatgtgttatcagagcatgtaactttgaattgtgtgacaacccttttctgtgttctaa
accatgggtacacagacacatactatgatattcgataatgcatttaattgcactttcagtagacatactgatgccctttcgc
ttgatgtttcagaaaagtcaggtaattttaaacacttacgagagttgtgtttaaaaataaagatgggtttctctatgtttataa
gggctatcaacctatagatgtagttcgtgatctaccttctggttttaaacactttgaaacctatttttaagttgcctcttggtatta
acattacaatttttagagccattcttacagcctttcacctgctcaagacatttggggcacgtcagctgcagcctattttgtt
ggctatttaaaagccaactacatttatgctcaagtatgatgaaaatggtacaatcacagatgctgtgtgtgttctcaaaatcc
actgtcgaactcaaatgctctgttaagagctttgagattgacaaaaggaattaccagaccttaatttcagggtgtgtccct
caggagatgtgtgagattccctaattacaaactgtgtccttttggagaggttttaattgctactaaattcccttctgtcta
tgcatggggagagaaaaaaatttctaattgtgtgtgtgattactctgtgtctcaactcaacattttttcaacctttaagt
ctatggcgtttctgccactaagtgaatgatctttgtcttccaatgtctatgcagattctttttagtcaagggagatgatgt
aagacaaatagcgccaggacaaactggtgttatgtgtgattataattataaattgccagatgattcatgggtgtgtcctt
gcttggaaactaggaacattgatgctacttcaactggaattataattataaataaggtatcttagacatggcaagcttag
gccctttgagagagacatactaatgtgcctttctccctgatggcaaaccttgacccccacctgtcttaattgttattggc
cattaaatgattatggttttacaccactactggcattggctaccaaccttacagagttgttagtactttcttgaacttttaaat
gcaccggccacgggtttgtggacccaaaattaccactgaccttataagaaccagtggtgcaattttaatttaaggactca
ctggtactggtgtgttaactccttctcaagagatttcaaccttcaacaatttggccgtgatgtttctgatttactgattc
cgttcgagatcctaaaacatctgaatattagacatttcaaccttgccttttgggggtgaagtgaattacacctggaaca
aatgcttcatctgaagtgtgttctatatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcac
accagcttggcgcatatatttacttgaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcg
acatttctatgagtcgacatttctatiggagctggcatttgtgctagtaccatacagtttctttattacgtagtactagcc
aaaaatctattgttgcttatactatgtcttttaggtgtgatagttcaattgcttactctaataacaccattgtctatacctactaa
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aacaggatcgcaacacacgtgaagtgttcgtcaagtcaacaatgtacaaaacccaactttgaatatatttgggtgtg
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ctcgtgatgtgtgctcatgaagcaaatatggcgaaatgcctaggtgatattaatgctagagatctcatttgcgcagaag
ttcaatggacttacagtggtccacctgtgtcactgatgatattgtgtgctcactgctgtctagttagtggtactgc
cactgtggtatggacatttgggtgtggtgtgtcttcaaataccttttctatgcaaatggcatataggtcaatggcatt
ggagttacccaaatgttctctatgagaacaaaaaacaatcgcaaccaatttaacaaggcgattagtaaatcaaga
atcacttacaacaacatcaactgcattgggcaagctgcaagacgttgtaaccagaatgtcgaagcatttaaacacacttg
ttaacaacttagctctaattttgtgtcaatttcaagtgtgtcaaatgatactcctttcgcgacttgataaagtcaggcgggag
gtacaaattgacaggttaattacaggcagacttcaaagccttcaaacctatgtaacacaacaactaatcagggtgtgtga
aatcagggtcttctgctaatttctgtgtactaaaaatgtctgagtggtgttcttgacaatcaaaaagagtgactttgtggaa
agggtaccacctatgtccttccacaagcagcccgcatggtgtgtcttctcatgtcacgtatgtgccatcccag
gagaggaaactcaccacagcgccagcaatttgcattgaaggcaagcatacttccctcgtgaagggtttttgtgttaat
ggcacttcttggttattacacagaggaaacttcttccacaaataattactacagacaatacattgtctcaggaaattgt
gatgtcgttattggcatcaaaacacagtttatgatcctctgcaacctgagctcgactcattcaagaagagctggac
aagtacttcaaaaatcatacatcaccagatgttgatcttggcgacatttcaggcattaacgcttctgtcgtcaacattcaaa

aagaaattgaccgctcaatgaggtcgctaaaaatttaaatgaatcactcattgaccttcaagaattgggaaaatatgag
caatatattaaatggccttggtatgttggtcggcttcattgctggactaattgccaicgtcatggttacaatcttgdtgtt
gcatgactagtgtgagttgcctcaagggtgcatgctctgtgtgttcttgctgcaagttgatgaggatgactctgagcc
agttctcaagggtgtcaattacattacataa

SEQ ID NO: 2 - Protein sequence for full length S-protein from accession number AAP13441 corresponding to the gene AY278741 (1256aa)

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRS
DTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG
WVFGSTMNNKSQSVIINNSTNVVIRACNFELCDNPFFAVSKPMGTQHTM
IFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPI
DVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVG
YLKPTTFMLKYDENGTTTDAVDCSQNPLAELKCSVKSFEDKGIYQTSNFR
VVPBGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLY
NSTFFSTFKCYGVSATKLNLCFSNVYADSFVVKGDDVRQIAPGQTGVIA
DYNKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDI
SNVPFSPDGKPCPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFELLNA
PATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSD
FTDSVRDPKTSEILDSPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTA
IHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYH
TVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMA
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVF
AQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTADAGF
MKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTAT
AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS
QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL
DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG
KAYFPREGVVFVNGTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVY
DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVA
KNLNEIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTILLCCMTSCC
SCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT

**SEQ ID NO: 3 - Protein sequence for Spike protein amino acid 275-1081
from accession number AAP13441 (807aa) (wild type, wt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFNPITNLC
PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK
LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
WNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALN
CYWPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNO
CVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP
CSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN
NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYT
MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE
CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG
GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
QMA YRFNGIGVTQNVLYENQKQIANQFNKAISQKESLTTTSTALGKLQDV
VNQNAQALNTLVKQLSSNFGAIVSLNDILSRDKVEAEVQIDRLITGRLQS
LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFP
QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

**SEQ ID NO: 4 - Protein sequence for Spike protein amino acid 275-1081
mutant with 9 potential N-linked glycosylation sites eliminated
(807aa)(substituted Alanine shown as "a")(mutant, mt):**

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPSPGDVVRFPNlaNLCP
FGEVFaATKFPSVYAWERKKISNCVADYSVLYNsaFFSTFKCYGVSATKLN
DLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN
TRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCY
WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCV
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCS
FGGVSVITPGTNaSEVAVLYQDVaCTDVSTAIHADQLTPAWRIYSTGNNV
FQTQAGCLIGAEHVDTSYECDIPGAGICASYHTVSLRSTSQKSIVAYTMS
LGADSSIAYSaNTIAIPTNFaISITTEVMPVSMAKTSVDCNMYICGDSTECAN
LLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFN
FaQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ
KFNGLTVLPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQM
AYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVN
QNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQ
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQA
APHGVVFLHVTYVPSQERNFaTAPAICHEGKAYFPREGVVFVFN

SEQ ID NO: 5 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with native virus codons and elimination of N-glycosylation sites (2421bp) (substituted nucleotides shown capitalized):

gctgttgattgttctcaaaatccacttgctgaactcaaagctctgttaagagctttgagattgacaaaggaatttacc
agacctctaatttcagggtgttcctcaggagatgtgtgagattccctaattGcaaacttggtcctttggagagggtt
ttGCCGctactaaattcccttctgtctatgcatgggagagaaaaaatttctaattgtgtgctgattactctgtgctcta
caactcaGcattttttcaacctttaagtgtatggcgtttctgccactaagtgaatgatcttctctccaatgtctatgca
gattctttttagtcaaggagatgatgaagacaaatagcgccaggacaaactgggtgtattgctgattataattataaat
tgcagatgattcatgggtgtgcttctgtgaatactaggaacattgatgctactcaactggtattataattataaat
ataggatcttagacatggcaagcttaggccctttgagagagacatatctaagtgcctttctccctgatggcaaacctt
gcacccacctgctcttaattgttattggccattaaatgattatggttttacaccactactggcattggctaccaaccttaca
gagttgtagtacttctttgaacttttaaatgcaccggccacgggttgtggacaaaattatccactgaccttataagaac
cagtgtgtcaattttaatttaattggactcactgggtactgggtgttaactccttctcaagagatttcaaccatttcaacaat
ttggcgtgatgtttctgaattcactgaattccgttcgagatcctaaacatctgaafattagacaattcaccttgccttttg
gggtgaagtgaattacacctggaacaaatgctGcatcgaagtgtgttctatcaagatgttGCctgcactgatg
ttttacagcaattcatgcagatcaactcacaccagcttggcgcatattctactggaacaaatgattccagactcaag
caggctgtcttataggagctgagcatgtcgacacttctatgagtcgacattcctattggagctggcattgtgchgta
ccatacagttctttattacgtagtactagccaaaaatctatttggcttatactatgtcttttaggtgctgatagtcaattgctt
actctGCCaacaccattgctatacctactaactttGcaattagcattactacagaagtaatgcctgttttatggctaaaa
cctccgtagattgtaatatgtacatctgcggagattctactgaatgtgctaattgcttctccaatatggtagcttttcacac
aactaaatcgtgcactctcaggtattgtgctgaacaggatcgcaacacacgtgaagtgttcgctcaagtcaaacaaat
gtacaaaaccccaactttgaaatatttgggtgttttaattttGcacaatattacctgacctttaaagccaactaagagg
tctttattgaggacttgctctttaataaggtgacactcgctgatgctggcttcagaaagcaatatggcgaatgcctagggtg
atattaatgctagagatctcattgtgcgcagaagttcaatggacttacagtggtgccacctctgctcactgatgatgatt
gtgcctacactgtgctctagttagtggtactgccactgctggatggacatttgggtgctggcgctgctcttcaaatacctt
ttgctatgcaaatggcatatagggtcaatggcattggagttacccaaaatgttctctatgagaacaaaaacaaatcgcca
accaatttaacaaggcgattagtcaaatcaagaatcacttacaacaacatcaactgcattgggcaagctgaagacgtt
gttaaccagaatgtcaagcattaaacacactgttaacaacttagctctaatttgggtgcaatttcaagtgtgctaaatga
tacccttgcgacttgataaagtcgaggcggaggtacaaattgacagggttaattacaggcagacttcaaaagccttcaaa
cctatgtaacacaacaactaatcagggtgctgaaatcagggtcttctgctaatcttgcgtactaaaaatgtctgagtgtg
tcttgacaatcaaaaagagttgacttttgggaaagggtaccaccttatgtccttccacaagcagccccgatgggtg
ttgtctctacatgtcacgtatgtgccatccaggagaggaaacttcGccacagcgccagcaatttgcataagggcaa
agcatacttccctgtgaagggtgttttgtgttaattggc

SEQ ID NO: 6 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with altered codon usage to enhance expression and elimination of N-glycosylation sites (2421bp):

GCCGTGGACTGCTCCCAGAACCCCTGGCCGAGCTGAAGTCTCCGTGAAGT
CCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGGTGCCCTC
CGGCGACGTGGTGCGCTTCCCCAACATCGCCAACCTGTGCCCTTCGGCGAGGTG
TTCGCCGCCACCAAGTTCCCCTCCGTGTACGCCTGGGAGCGCAAGAAGATCTCCA
ACTGCGTGGCCGACTACTCCGTGCTGTACAACCTCCGCCTTCTTCTCCACCTTCAA
GTGCTACGGCGTGTCCGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTAC
GCCGACTCCTTCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCCGGCCAGA
CCGGCGTGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCATGGGCTGCGT
GCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACAACCTAC
AAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCCTTCGAGCGCGACATCTCCA
ACGTGCCCTTCTCCCCGACGGCAAGCCCTGCACCCCCCGCCCTGAAGTCTGCTA
CTGGCCCCCTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCC
TACCGCGTGGTGGTGTCTTTCGAGCTGCTGAACGCCCCCGCCACCGTGTGCG
GCCCCAAGCTGTCCACCGACCTGATCAAGAACCAGTGCCTGAACCTTCAACTTCAA
CGCCCTGACCGGCACCGCGTGTGACCCCCCTCCTCCAAGCGCTTCCAGCCCTTC
CAGCAGTTCGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCCAAGA
CCTCCGAGATCCTGGACATCTCCCCCTGCTCCTTCGGCGGCGTGTCCGTGATCAC
CCCCGGCACCAACGCCGCTCCGAGGTGGCCGTGCTGTACCAGGACGTGGCCTGC
ACCGACGTGTCCACCGCCATCCACGCCGACGCTGACCCCCGCTGGCGCATCT
ACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATCGGCGCCGA
GCAGTGGACACCTCCTACGAGTGCAGATCCCCATCGGCGCCGGCATCTGCGCC
TCCTACCACACCGTGTCCCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCT
ACACCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGC
CATCCCCACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCCGTGTCCATG
GCCAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGC
CCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTC
CGGCATCGCCGCGAGCAGGACCGCAACACCCGCGAGGTGTTGCGCCAGGTGAAG
CAGATGTACAAGACCCCCACCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAGA
TCCTGCCGACCCCTGAAGCCACCAAGCGCTCCTTCATCGAGGACCTGCTGTT
CAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTACGGCGAGTGCCTG
GGCGACATCAACGCCCCGCGACCTGATCTGCGCCAGAAAGTTCAACGGCCTGACCG
TGCTGCCCCCCTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAGATC
CCCTTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACG
TGCTGTACGAGAACCAGAAGCAGATCGCCAACCAAGTTCAACAAGGCCATCTCCCA
GATCCAGGAGTCCCTGACCAACACCTCCACCGCCCTGGGCAAGCTGCAGGACGTG
GTGAACCAGAACGCCCAGGCCCTGAACACCTGGTGAAGCAGCTGTCTTCAACT
TCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGA
GGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCGCCTGCAGTCCCTGCAGACC
TACGTGACCCAGCAGCTGATCCGCGCCGCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCCTGCTGGGCCAGTCCAAGCGCGTGGACTTCTG
CGGCAAGGGCTACCACCTGATGTCTTCCCCAGGCCGCCCCCACGGCGTGGTG
TTCCTGCACGTGACCTACGTGCCCTCCCAGGAGCGCAACTTCGCCACCGCCCCCG
CCATCTGCCACGAGGGCAAGGCCCTACTTCCCCGCGAGGGCGTGTTCGTGTTCAA
CGGC

SEQ ID NO: 7 - Potential N-glycosylation sites within the protein sequence of the Spike protein amino acid 275-1081 (807aa) (wild type, wt) with potential N-glycosylation sites underlined.

AVDCSQNPLAELKCSVKSF¹EDKGIYQTSNFRVVP²SGDVVRFP³NITNLC
 PFGEVFNATK⁴FPSVYAWERKKISNCVADYSVL⁵YNSTFFSTFKCYGVSATK
 LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
 WNTRNIDATSTGN⁶YNYKYRYLRHGKLRP⁷FERDISNVPFSPDGK⁸PCTPPALN
 CYWPLNDYGFYTTT⁹GIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQ
 CVN¹⁰FNFNGLTGTGVLTPSSKRFQPFQ¹¹QFGRDVSDF¹²TDSVRDPKTSEILDIS
 CSF¹³GGVSVITPGT¹⁴NA¹⁵SEVAVLYQDV¹⁶NCTDVSTAIHADQLTPAWRIYSTGN
 NVFQTQAGCLIGAEHVDTSYEC¹⁷DIPIGAGICASYHTVSL¹⁸LRSTSQKSIVAYT
 MSLGADSSIAYSNNTIAIPTN¹⁹FSISITTEVM²⁰PVSMAKTSVDCNMYICGDSTE
 CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLK²¹YFG
 GFN²²FSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
 CAQKFNGLT²³VL²⁴PPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
 QMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDV
 VNQNAQALNTLVKQLSSNFGA²⁵ISSVLNDILSR²⁶LDKVEAEVQIDRLITGRLQS
 LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSMFP
 QAAPHGVVFLHVTYVPSQERN²⁷FTTAPAI²⁸HEGKAYFPREGVVFVNG

SEQ ID NO: 8 Amino acid sequence of Region II peptide

VLYN¹SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKLPDDFMGCVLAWNTRNIDATSTGN²YNYKYRYLRHGKLRP³FERDISNVPFSP
 DGK⁴PCTPPALNCYWPLNDYGFYTTT⁵GIGYQPYRVVLSFELLNAPATVCGPKLST
 DLIKNQCVN⁶FNFNGLTGTGVLTPSSKRFQPFQ⁷QFGRDVSDF⁸TDSVRDPKTSEILDIS
 PCSF⁹GGVSVITPGTNAASEVAVLYQDV

SEQ ID NO: 9 Amino acid sequence of Region III peptide

AEQDRNTREVFAQVKQMYKTPTLK¹YFGGFNFAQILPDPLKPTKRSFIEDLLFNKV
 TLADAGFMKQYGECLGDINARDLICAQKFNGLT²VL³PPLLTDDMIAAYTAALVSGT
 ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQ
 ESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGA⁴ISSVLNDILSR⁵LDKVEAEV
 QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG
 YHL

SEQ ID NO: 10 Amino acid sequence of Region IV peptide

VLYN¹SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKLPDDFMGCVLAWNTRNIDATSTGN²YNYKYRYLRHGKLRP³FERDISNVPFSP
 DGK⁴PCTPPALNCYWPLNDYGFYTTT⁵GIGYQPYRVVLSFELLNAPATVCGPKLST
 DLIKNQCVN⁶FNFNGLTGTGVLTPSSKRFQPFQ⁷QFGRDVSDF⁸TDSVRDPKTSEILDIS
 PCSF⁹GGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQLTPAWRIYSTGNNVF

QTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSS
IAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCT
QLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRS
FIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIA
AYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIA
NQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI
LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ
SKRVDFCGKGYHL

SEQ ID NO: 11 Amino acid sequence of Region II peptide from Spike protein from accession number AAP13441(wild type)

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQ
TGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRP
FERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSF
ELLNAPATVCGPKLSTD LIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFG
RDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDV

SEQ ID NO: 12 Amino acid sequence of Region III peptide from Spike protein from accession number AAP13441(wild type)

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIED
LLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMI
AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYEN
QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF
GAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASAN
LAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 13 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG
VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFE
RDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFEL
LNAPATVCGPKLSTD LIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRD
VSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDV
STAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICA
SYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVS
MAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE
VFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADA
GFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGT
ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA
ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILS
RLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV
LGQSKRVDFCGKGYHL

SEQ ID NO: 14 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNLCPFGEVFNATKFPSPVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPCSEGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPLLTDDMLAAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 15 Linker for nucleotide primer oligo #1

TCGCTCGAGAAAAGAGTGCTCTACAACCTCAGCATTT

SEQ ID NO: 16 Linker for nucleotide primer oligo #2

ATCTCTAGATTAAACATCTTGATATAGAACAGC

SEQ ID NO: 17 Linker for nucleotide primer oligo #3 TCGCTCGAG

AAAAGAGCTGAACAGGATCGCAACACA

SEQ ID NO: 18 Linker for nucleotide primer oligo #4

ATCTCTAGATTAAAGGTGGTAGCCCTTTCC

SEQ ID NO: 19 SARS Spike Glycoprotein Fragment synthetic DNA sequence with N-lined glycosylation site mutations (2421 bp)

GCCGTGGACTGCTCCCAGAACCCACTGGCCGAGCTGAAGTGCTCCGTGAAGTCCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGCGCCATCCGGCGACGTGGTGCGCTTCCCAAACATCGCCAACCTGTGCC

CATTCGGCGAGGTGTTTCGCCGCCACCAAGTTCCCATCCGTGTACGCCTG
GGAGCGCAAGAAGATCTCCAACCTGCGTGGCCGACTACTCCGTG
CTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCCGC
CACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCG
TGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGGCGT
GATCGCCGACTACAACTACAAGCTGCCAGACGACTTCATGGGCTGCGTG
CTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACA
ACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGAGCG
CGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCAC
CAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACACCACC
ACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGTCTCTTCGAGC
TGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCGACCT
GATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACC
GGCGTGCTGACCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCGG
CCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACCT
CCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGCGTGTCCGTGATC
ACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGACG
TGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCC
GGCTGCCTGATCGGCGCCGAGCACGTGGACACCTCCTACGAGT
GCGACATCCCAATCGGCGCCGGCATCTGCGCCTCCTACCACACCGTGTC
CCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCTACACCATGTCCC
TGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCA
ACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCAGTGTCCATGGC
CAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAG
TGCGCCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCG
CGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTG
TTCGCCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTTCG
GCGGCTTCAACTTCGCCCAGATCCTGCCAGACCCACTGAAGCCAACCAA
GCGCTCCTTCATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGAC
GCCGGCTTCATGAAGCAGTACGGCGAGTGCCTGGGCGACATCAACGCCC
GCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCGTGCTGCCACC
ACTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGTGTC
CGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAG
ATCCCATTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGAC
CCAGAACGTGCTGTACGAGAACCAGAAGCAGATCGCCAACCAGTTCAAC
AAGGCCATCTCCAGATCCAGGAGTCCCTGACCACCACCTCCACCGCCCT
GGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCCCT
GAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTOCTCCG
TGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCA
GATCGACCGCCTGATCACC GGCCGCTGCAGTCCCTGCAGACCTACGTG
ACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGGACTTCTGCGGCAAGGGCTACCACCTGATGTCTTCCCACAGGCC
GCCCCACACGGCGTGGTGTTCTTCTGCACGTGACCTACGTGCCATCCCAGG
AGCGCAACTTCGCCACCGCCCCAGCCATCTGCCACGAGGGCAAGGCCTA
CTTCCCACGCGAGGGCGTGTTCTGTGTTCAACGGC

SEQ ID NO: 20

SARs Spike glycoprotein Fragment I protein sequence without the N-linked glycosylation sites (807 amino acids encoded by SEQ ID NO: 19):

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSGDVVRFPNIANLCPFGEVFAATKFPSVYA
WERKKISNCVADYSVLVNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGV
IADYNYKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPT
PALNCYWPLNDYGFTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTG
TGVLTSSSRKFQPFQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQ
DVACTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSL
RSTSQKSIVAYTMSLGADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANL
LLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFI
EDLLFNKVTADAGFMKQYGECLGDINARDLCAQKFNGLTVLPPLLTDMDIAAYTAALVSGTATA
GWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQ
DVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQAAPHGVVFLHVTYVPSQERNFATAPAI
CHEGKAYFPREGVVFVNG

SEQ ID NO: 21: SARs Spike glycoprotein Fragment II synthetic DNA sequence with N-linked glycosylation site mutations (744bps):

GTGCTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTC
CGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCT
TCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGG
CGTGATCGCCGACTACAACTACAAGCTGCCAGACGACTTCATGGGCTGC
GTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACT
ACAACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGA
GCGCGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACC
CCACCAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACAC
CACCACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGTCTCCTTC
GAGCTGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCG
ACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGC
ACCGGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTT
CGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACC
TCCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGCGTGCTCCGTGAT
CACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGAC
GTG

SEQ ID NO: 22: SARs Spike glycoprotein Fragment II protein sequence without the N-linked glycosylation sites (248 amino acids, encoded by SEQ ID 21):

VLVNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVADYNYKLPDDFMG
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSSRKFQPF
QQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDV

SEQ ID NO: 23: SARS Spike glycoprotein Fragment III synthetic DNA sequence with N-linked glycosylation site mutations (834 bps):

GCCGAGCAGGACCGCAACACCCGCGAGGTGTTGCCCCAGGTGAAGCAGA
TGTAACAAGACCCCAACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAG
ATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTCATCGAGGACCT
GCTGTTCAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTAC
GGCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCCAGA
AGTTCAACGGCCTGACCGTGCTGCCACCACTGCTGACCGACGACATGAT

CGCCGCCTACACCGCCGCCCTGGTGTCCGGCACCGCCACCGCCGGCTGG
ACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCATTCCGCCATGCAGATGG
CCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAA
CCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCCAGATCCAG
GAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGG
TGAACCAGAACGCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCCTC
CAACTTCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGG
ACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCCGCT
GCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAG
ATCCGCGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCGTGC
TGGGCCAGTCCAAGCGCGTGGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 24: SARs Spike glycoprotein Fragment III protein sequence without the N-linked glycosylation sites (278 amino acids, encoded by SEQ ID NO: 23):
AEQDRNTREVFQVQKMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQ
YGECLGDINARDLICAQKFNGLTVPPLLTDMDIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS
SNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHL

SEQ ID NO: 25: SARs Spike glycoprotein Fragment IV synthetic DNA sequence with N-linked glycosylation site mutations (2034 bps):

GTGCTGTACAACTCCGCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCCGCCACCAAGCT
GAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCGTGGTGAAGGGCGACGACGTG
CGCCAGATCGCCCCAGGCCAGACCGGCGTGATCGCCGACTACAACTACAAGCTGCCAGAC
GACTTCATGGGCTGCGTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCA
ACTACAACCTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGAGCGCGACAT
CTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCACCAGCCCTGAACTGCTAC
TGGCCACTGAACGACTACGGCTTCTACACCACCAACCGGCATCGGCTACCAGCCATACCGCG
TGGTGGTGCTGTCTTCGAGCTGCTGAACGCCCGCCAGCCACCGTGTGCGGCCCAAAGCTGTC
CACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACCGGC
GTGCTGACCCCATCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCCGGCCGCGACGTGTCCG
ACTTCACCGACTCCGTGCGCGACCCAAAGACCTCCGAGATCCTGGACATCTCCCCATGCTC
CTTCGGCGGCGTGCTCGGTGATCACCCAGGCACCAACGCCGCTCCGAGGTGGCCGTGCT
GTACCAAGGACGTGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACGAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATC
GGCGCCGAGCAGTGACACCTCTACGAGTGCGACATCCCAATCGGCGCCGCGCATCTGC
GCCTCTACCACACCGTGCTCCTGCTGCGCTCCACCTCCAGAAAGTCCATCGTGGCC TACA
CCATGTCCCTGGGCGCGGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCAAC
CAACTTCGCCATCTCCATCACCAACCGAGGTGATGCCAGTGTCATGGCCAAGACCTCCGTG
GACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCGCCAACCTGCTGCTGCAGTACG
GCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCA
ACACCCGCGAGGTGTTCCGCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTT
CGGCGGCTTCAACTTCGCCAGATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTC
ATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGACGCGGCTTCATGAAGCAGTACG
GCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCAGAAGTTCAACGGCC
TGACCGTGCTGCCACCACTGCTGACCGACGACATGATCGCCGCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCAT
CGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAAGCTGCTGTACGAG
AACCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCAGATCCAGGAGTCCCTGA
CCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGGTGAACCAGAAGCGCCAGGCC
TGAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTCCTCCGTGCTGAACGA
CATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGG
CCGCTGCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAGATCCG
CGCCTCCGCCAACCTGGCCGCCACCAAGATGTCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 26: SARs Spike glycoprotein Fragment IV protein sequence without the N-linked glycosylation sites (678 amino acids, encoded by SEQ ID NO: 25):
VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMG
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSKRFQPF
QQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQ
LTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSL
GADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA
LSGIAAEQDRNTREVFQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAG
FMKQYGECLGDINARDLCAQKFNGLTVLPPLLTDMDIAAYTAALVSGTATAGWTFGAGAALQIPF
AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLV
KQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE
CVLGQSKRVDFCGKGYHL